Abstract

A method of predicting a scaffold of a protein comprising a query sequence, wherein said method uses a database which contains environmental information on the side chain of each amino acid residue contained in the amino acid sequence of each reference protein whose three-dimensional structure is known or predictable, and wherein said method comprises the step of: conducting matching based on the environmental information on each amino acid residue of each reference protein and hydrophobicity or hydrophilicity property of the side chain of each amino acid residue of the query sequence, and choosing at least one template protein among the reference proteins that has high similarity in three-dimensional structure to the protein comprising the query sequence.